WE CLAIM:

1. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with residues 24-292 of SEQ. ID No. 1.

2. A composition according to claim 1 wherein at least a portion of the protein has at least 95% identity with residues 24-292 of SEQ. ID No. 1.

3. A composition according to claim 1 wherein at least a portion of the protein comprises consecutively of residues 24-292 of SEQ. ID No. 1.

4. A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5. A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

6. A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å, α =90.0°, β =92.2°, and γ =90.0°.

7. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice in a $P2_1$ space group.

8. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å, α =90.0°, β =92.2°, and γ =90.0°.

9. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with residues 24-258 of SEQ. ID No. 1.

10. A composition according to claim 9 wherein at least a portion of the protein has at least 95% identity with residues 24-258 of SEQ. ID No. 1.

11. A composition according to claim 9 wherein at least a portion of the protein comprises consecutively of residues 24-258 of SEQ. ID No. 1.

12. A composition according to claim 9 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

13. A composition according to claim 9 wherein the protein crystal has a crystal lattice in a $P3_121$ space group.

14. A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å, α =90.0°, β =90.0°, and γ =120°.

15. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice in a $P3_121$ space group.

16. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å, α =90.0°, β =90.0°, and γ =120°.

17. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with residues 24-267 of SEQ. ID No. 1.

18. A composition according to claim 17 wherein at least a portion of the protein has at least 95% identity with residues 24-267 of SEQ. ID No. 1.

19. A composition according to claim 17 wherein at least a portion of the protein comprises consecutively of residues 24-267 of SEQ. ID No. 1.

20. A composition according to claim 17 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

21. A composition according to claim 17 wherein the protein crystal has a crystal lattice in a $P4_12_12$ space group.

22. A composition according to claim 17 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=114 Å, b=114 Å, c=157 Å, α =90°, β =90°, and γ =90°.

23. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice in a $P4_12_12$ space group.

24. A composition comprising HSD11B1 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=114 Å, b=114 Å, c=157 Å, α =90°, β =90°, and γ =90°.

25. A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 24-292 of SEQ. ID No. 1; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

26. A method according to claim 25 wherein the protein has at least 95% identity with residues 24-292 of SEQ. ID No. 1.

27. A method according to claim 25 wherein at least a portion of the protein comprises consecutively of residues 24-292 of SEQ. ID No. 1.

28. A method according to claim 25 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

29. A method according to claim 25 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

30. A method according to claim 29 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å, α =90.0°, β =92.2°, and γ =90.0°.

31. A method according to claim 25 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å, α =90.0°, β =92.2°, and γ =90.0°.

32. A method according to claim 25, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

33. A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 24-258 of SEQ. ID No. 1; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

34. A method according to claim 33 wherein the protein has at least 95% identity with residues 24-258 of SEQ. ID No. 1.

35. A method according to claim 33 wherein at least a portion of the protein comprises consecutively of residues 24-258 of SEQ. ID No. 1.

36. A method according to claim 33 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

37. A method according to claim 33 wherein the protein crystal has a crystal lattice in a $P3_121$ space group.

38. A method according to claim 37 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å, α =90.0°, β =90.0°, and γ =120°.

39. A method according to claim 33 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å, α =90.0°, β =90.0°, and γ =120°.

40. A method according to claim 33, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

41. A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 24-267 of SEQ. ID No. 1; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

42. A method according to claim 41 wherein the protein has at least 95% identity with residues 24-267 of SEQ. ID No. 1.

43. A method according to claim 41 wherein at least a portion of the protein comprises consecutively of residues 24-267 of SEQ. ID No. 1.

44. A method according to claim 41 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

45. A method according to claim 41 wherein the protein crystal has a crystal lattice in a $P4_12_12$ space group.

46. A method according to claim 45 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=114 Å, b=114 Å, c=157 Å, α =90°, β =90°, and γ =90°.

47. A method according to claim 41 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=114 Å, b=114 Å, c=157 Å, α =90°, β =90°, and γ =90°.

48. A method according to claim 41, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

49. A composition comprising an isolated protein consisting of residues 24-292 of SEQ. ID No. 1.

50. A composition according to claim 49 wherein the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

51. A composition comprising an isolated protein consisting of residues 24-258 of SEQ. ID No. 1.

52. A composition according to claim 51 wherein the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 3.

53. A composition comprising an isolated protein consisting of residues 24-267 of SEQ. ID No. 1.

54. A composition according to claim 53 wherein the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 4.

55. A composition comprising an isolated protein consisting of SEQ. ID No. 5.

56. A composition comprising an isolated protein consisting of SEQ. ID No. 6.

57. A composition comprising an isolated protein consisting of SEQ. ID No. 7.

58. A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with residues 24-292 of SEQ. ID No. 1; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

59. A method according to claim 58 wherein at least a portion of the protein has at least 95% identity with residues 24-292 of SEQ. ID No. 1.

60. A method according to claim 58 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å, α =90.0°, β =92.2°, and γ =90.0°.

61. A method according to claim 58, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

62. A method according to claim 58, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

63. A method according to claim 58, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

64. A method according to claim 58, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

65. A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with residues 24-258 of SEQ. ID No. 1; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

66. A method according to claim 65 wherein at least a portion of the protein has at least 95% identity with residues 24-258 of SEQ. ID No. 1.

67. A method according to claim 65 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å, α =90.0°, β =90.0°, and γ =120°.

68. A method according to claim 65, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

69. A method according to claim 65, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

70. A method according to claim 65, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

71. A method according to claim 65, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

72. A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with residues 24-267 of SEQ. ID No. 1; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

73. A method according to claim 72 wherein at least a portion of the protein has at least 95% identity with residues 24-267 of SEQ. ID No. 1.

74. A method according to claim 72 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=114 Å, b=114 Å, c=157 Å, α =90°, β =90°, and γ =90°.

75. A method according to claim 72, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

76. A method according to claim 72, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

77. A method according to claim 72, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

78. A method according to claim 72, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.